

Figure 1A

1 CCACGCGTCCGATAATTACTAAGTACAGGGTCCCAAATAGAACTCTATTCCAACCTTAAAG 60
 61 GACAAGAAAAAAGTCCAAGATTACCCAGTGAACATAGTTTGTAGTTTGTGTCAACAA 120
 121 ACTGATAGTCACGCCTAATTTCTTCTATACTCCATAAAGACAGTGTGTATGTATGTGT 180
 181 GTGTGTTTCTTTGTGTGTATGTATGTATTTCAGGTATATGTGTATAGCCCTTAGCTAGGAGA 240
 241 CAATCTAGTTTATCTAAAGGCTTATTTGAGCCCTTCTCACGTTTCATTTATTTTATTTA 300
 301 ATAAGCATTATATATCAGGTATTATTCAAAGCTCTTTAGAAATCTTTAGACATATTAACC 360
 361 CATATAATTCTCTTCTCTATAGGGAATAGATATGATTATTTATGCTATTTTATGGATGAT 420
 421 GAAGCTTTCTAAACATGTTATAGCCAGTAAGTGTTACTATCTCTCATTCCTATCTCTGT 480
 481 TCTATCTTGTTCTCTCCAGATAATGTGATACTATGTGGAGGTTTCTGACCACAGAGAATGT 540
 1 M S 2
 541 CCAGCACTCTTGGCCACAACATGGAATCTCCTCATCACACTGATGTTGACCCCTTCTGTCT 600
 3 S T L G H N M E S P H H T D V D P S V F 22
 601 TCTTCTCTTGGGCATCCCAGGTCTGGAACAATTTTCATTTGTGGCTCTCACTCCCCTGTGT 660
 23 F L L G I P G L E Q F H L W L S L P V 42
 661 GTGGCTTAGGCACAGCCACAATTTGTGGGCAATATACTATTCTGGTGTGTGTGCCACTG 720
 43 G L G T A T T I V G N I T I L V V V A T E 62
 721 AACCAGTCTTGACACAAGCCTGTGTACCTTTTCTGTGTCATGCTCTCAACCATCGACTTGG 780
 63 P V L H K P V Y L F L M L S T I D L A 82
 781 CTGCCCTGTCTCCACAGTTCCCAAGCTACTGGCTATCTTCTGGTGTGGAGCCGGACATA 840
 83 A S V S T V P K L L A I F W C G A G H I 102
 841 TATCTGCCCTCTGCCCTGGCCACATATGTTCTTCATTTCATGCCTTCTGCATGATGGAGT 900
 103 S A S A L A H M F F I H A F C M M E S 122
 901 CCACTGTGCTACTGGCCATGGCCTTTGATCGCTACGTGGCCATCTGCCACCCCATCCGCT 960
 123 T V L L A M A F D R Y V A I H P L R Y 142
 961 ATGCCACAATCCTCACTGACACCATCATTTGCCACATAGGGGTGGCAGCTGTAGTGGAG 1020
 143 A T I L T D T I I A H I G V A A V V R G 162

Figure 1B

1021 GCTCCCTGCTCATGCTCCCATGTCCCTTCTTTATTTGGGGCTTTGAACCTCTGCCAAAGCC 1080
 163 S L L M L P C P F F I G R L N F C Q S H 182

1081 ATGTGATCCTACACACGTACTGTGAGCACATGGCTGTGGTGAAGCTGGCCTGTGGAGACA 1140
 183 V I L H T Y █ E H M A V V K L A C G D T 202

1141 CCAGGCCTAACCGTGTGTATGGGCTGACAGCTGCACTGTGGTCATTTGGGGTTGACTTGT 1200
 203 R P N R V Y G L T A A L L V I G V D L F 222

1201 TTTGCATTGGTCTCTCCTATGCCCTAATGACACAAGCTGTCTTCGCCCTCTCATCCCATG 1260
 223 C I G L S Y A L I A Q A V L R L S S H E 242

1261 AAGCTCGGTCCAAGGCCCTAGGGACCTGTGGTTCCCATGCTGTGTATCCTCATCTCTTT 1320
 243 A R S K A L G T █ G S H V C V I L I S Y 262

1321 ATACACCAGCCCTCTTCTCCTTTTTTACACACCGCTTTGGCCATCACGTTCCAGTCCATA 1380
 263 T P A L F S F F T H R F G H H V P V H I 282

1381 TTCACATCTTTTGGCCAATGTTTATCTGCTTTTGCCACCTGCTCTTAATCCTGTGGTAT 1440
 283 H I L L A N V Y L L L P P A L N P V V Y 302

1441 ATGGAGTTAAGACCAACAGATCCGTAAAAGAGTTGTGAGGGTGTGTTCAAAGTGGGCAGG 1500
 303 G V K T K Q I R K R V V R V F Q S G Q G 322

1501 GAATGGGCATCAAGGCATCTGAGTGACCCCTGGAGTATAGAGGGACTTAATCCAAAAA 1560
 323 M G I K A S E 329

1561 AAAAAA 1567

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Figure 2

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Ra1c_GPCR      ~~~~~MSSNPTFA...PEMVGIPGLEBAHFWSPFLLSMYVAVAFENCLVYFVGR
prostate_GPCR ~~~~~MSSNPTFA...PEMVGIPGLEBAHFWSPFLLSMYVAVAFENCLVYFVGR
HGPRMY25      MSSTLGHMSPPHVDVDSVFFPGIPGLEQFLLHSLPFGGATATGNTLLVYGA
HOR_GPCR      MSDS...NLSTLHL...PDPEPLTGIPGLEBAHFWSPFLLSMYVAVAFENCLVYFVGR
MOR_GPCR      ~~~~~MAGQNTFHIAISFLLGIPGLENTFVWSPFLLSMYVAVAFENCLVYFVGR

Ra1c_GPCR      PERSLHAPMYLFLCMLAANDLALSSTPKLALFWPDSREISFACIOMPPFTHALSAI
prostate_GPCR PERSLHAPMYLFLCMLAANDLALSSTPKLALFWPDSREISFACIOMPPFTHALSAI
HGPRMY25      PEPVLEFMYLFLCMLSTIDLASVETPKLALFYCGAGHSASACLEMPFTHATCMN
HOR_GPCR      MNALHAPMYLFLCMLSTIDLASVETPKLALFLHAGESSSSCLACMPCSTFYAL
MOR_GPCR      LEPSLALPMSFECMLAPMSMCACSLALSLPFWDEHMRSEACIOMPPFTHALSAI

Ra1c_GPCR      ESTILLAMAFDRYVAICHLPLHAAVLANNVVGICGVALVRGSLFFFPPLIKRLAPCH
prostate_GPCR ESTILLAMAFDRYVAICHLPLHAAVLANNVVGICGVALVRGSLFFFPPLIKRLAPCH
HGPRMY25      ESTILLAMAFDRYVAICHLPLRYAIIITDITATIGCAVVRGSLMLPCFFISRLNRCQ
HOR_GPCR      ESTILLAMAFDRYVAICHLPLRYAIIITDITATIGCAVVRGSLMLPCFFISRLNRCQ
MOR_GPCR      ESAILLAMAFDRYVAICHLPLRYAIIITDITATIGCAVVRGSLMLPCFFISRLNRCQ

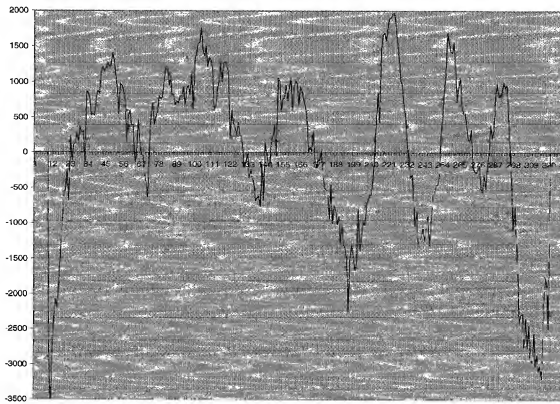
Ra1c_GPCR      SNVSEHYCVHQDVVKLAYDTLPLNVYGLTALLVMGVDMFSLSYLLIHSVLLLP
prostate_GPCR SNVSEHYCVHQDVVKLAYDTLPLNVYGLTALLVMGVDMFSLSYLLIHSVLLLP
HGPRMY25      SHVLLHYCEHMAVKLACDTRNRYVGLTALLVMGVDMFSLSYLLIHSVLLLP
HOR_GPCR      HRVLLHYCEHMAVKLACANITVNVYGLTALLVMGVDMFSLSYLLIHSVLLLP
MOR_GPCR      KYVLLHYCEHMAVKLACANITVNVYGLTALLVMGVDMFSLSYLLIHSVLLLP

Ra1c_GPCR      KSEPRKFEFCVSHIGVLAFYVPLGLSVVHRFNSLDEIVNVKGDVYLLLPVNVN
prostate_GPCR KSEPRKFEFCVSHIGVLAFYVPLGLSVVHRFNSLDEIVNVKGDVYLLLPVNVN
HGPRMY25      HEARSKALGTCSSHICVTLLSYVPAFSPFTHRFCHHVFVHTITLANNVYLLLPVNVN
HOR_GPCR      HDQKALGTCSSHICVTLLSYVPAFSPFTHRFCHHVEVKHTITLANNVYLLLPVNVN
MOR_GPCR      QNARSKALGTCVAHICVTLLAFYVPAFSPFTHRFCHHVFVHTITLANNVYLLLPVNVN

Ra1c_GPCR      ILYGAKTKOIRRVLAHFRISCDNDEA.GCNT
prostate_GPCR ILYGAKTKOIRRVLAHFRISCDNDEA.VGCK~
HGPRMY25      ILYGAKTKOIRRVLRVFSQGQMGKASE~
HOR_GPCR      ILYGAKTKOIRRVLRKILHLGK.TS~
MOR_GPCR      ILYGAKTKOIRRVVSLFQKQF~

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Figure 3



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Figure 4

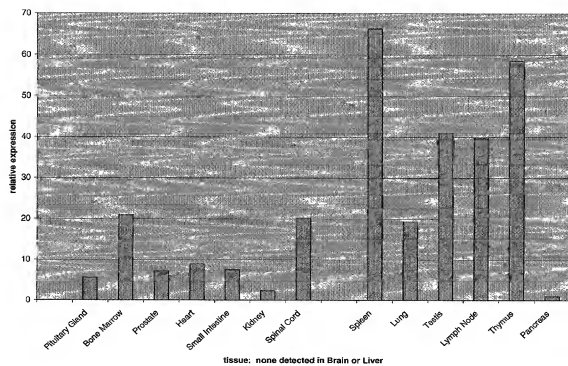


Figure 5.

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
rat G-protein coupled receptor, RA1c protein	gil3420759	52.83%	59.75%
human prostate specific G- protein coupled receptor, PSGR protein	gil11875778	51.89%	59.12%
human HOR 5'Beta14 protein	gil11908211	51.58%	60.76%
mouse MOR 3'Beta5 protein	gil11908222	54.95%	60.38%

Figure 6

